Phyre^2

Email	l.a.kelley@imperial.ac.uk
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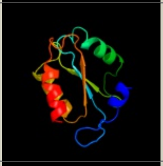
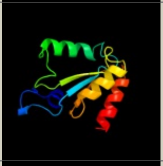
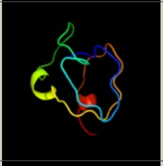
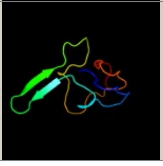
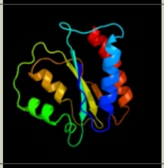
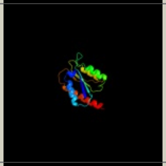
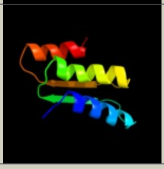
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3k3sG_	Alignment		100.0	98	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**altronate hydrolase; **PDBTitle:** crystal structure of altronate hydrolase (fragment 1-84) from shigella2 flexneri.
2	c3lazB_	Alignment		99.9	33	**PDB header:**lyase **Chain:** B: **PDB Molecule:**d-galactarate dehydratase; **PDBTitle:** the crystal structure of the n-terminal domain of d-2 galactarate dehydratase from escherichia coli cft073
3	c3frnA_	Alignment		89.8	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**flagellar protein flga; **PDBTitle:** crystal structure of flagellar protein flga from thermotoga maritima2 msb8
4	d1vmea1	Alignment		88.1	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
5	c1qd1A_	Alignment		82.1	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**formiminotransferase-cyclodeaminase; **PDBTitle:** the crystal structure of the formiminotransferase domain of2 formiminotransferase-cyclodeaminase.
6	c3ff1B_	Alignment		79.9	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** structure of glucose 6-phosphate isomerase from staphylococcus aureus
7	d2zdra1	Alignment		77.5	27	**Fold:**beta-clip **Superfamily:**AFP III-like domain **Family:**AFP III-like domain
8	c3hr4C_	Alignment		75.4	15	**PDB header:**oxidoreductase/metal binding protein **Chain:** C: **PDB Molecule:**nitric oxide synthase, inducible; **PDBTitle:** human inos reductase and calmodulin complex
9	d1c7qa_	Alignment		74.9	13	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
10	d1vlia1	Alignment		74.2	25	**Fold:**beta-clip **Superfamily:**AFP III-like domain **Family:**AFP III-like domain
11	c3g8rA_	Alignment		69.6	25	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**probable spore coat polysaccharide biosynthesis protein e; **PDBTitle:** crystal structure of putative spore coat polysaccharide biosynthesis2 protein e from chromobacterium violaceum atcc 12472

12	c3m7oB_	Alignment		67.2	21	**PDB header:**immune system **Chain:** B: **PDB Molecule:**lymphocyte antigen 86; **PDBTitle:** crystal structure of mouse md-1 in complex with phosphatidylcholine
13	c1tt9B_	Alignment		66.7	19	**PDB header:**transferase, lyase **Chain:** B: **PDB Molecule:**formimidoyltransferase-cyclodeaminase **PDBTitle:** structure of the bifunctional and golgi associated2 formiminotransferase cyclodeaminase octamer
14	c1xuzA_	Alignment		63.6	29	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**polysialic acid capsule biosynthesis protein siac; **PDBTitle:** crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
15	c2hnbA_	Alignment		60.8	18	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**protein mioc; **PDBTitle:** solution structure of a bacterial holo-flavodoxin
16	d1b1ca_	Alignment		57.7	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
17	c1vliA_	Alignment		55.7	26	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**spore coat polysaccharide biosynthesis protein spse; **PDBTitle:** crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
18	d2nu7b1	Alignment		53.4	13	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
19	c2q9uB_	Alignment		46.9	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**a-type flavoprotein; **PDBTitle:** crystal structure of the flavodiiron protein from giardia2 intestinalis
20	d1eucb1	Alignment		46.6	12	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
21	d1ja1a2	Alignment	not modelled	45.7	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
22	c3b8hA_	Alignment	not modelled	41.8	26	**PDB header:**biosynthetic protein/transferase **Chain:** A: **PDB Molecule:**elongation factor 2; **PDBTitle:** structure of the eef2-exoa(e546a)-nad+ complex
23	c2ohiB_	Alignment	not modelled	41.4	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**type a flavoprotein fpra; **PDBTitle:** crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state
24	d2f69a2	Alignment	not modelled	41.2	18	**Fold:**beta-clip **Superfamily:**SET domain **Family:**Histone lysine methyltransferases
25	c3hjbA_	Alignment	not modelled	40.1	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** 1.5 angstrom crystal structure of glucose-6-phosphate isomerase from2 vibrio cholerae.
26	c1ychD_	Alignment	not modelled	40.0	13	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nitric oxide reductase; **PDBTitle:** x-ray crystal structures of moorella thermoacetica fpra.2 novel diiron site structure and mechanistic insights into3 a scavenging nitric oxide reductase
27	c3tr5C_	Alignment	not modelled	38.9	26	**PDB header:**translation **Chain:** C: **PDB Molecule:**peptide chain release factor 3; **PDBTitle:** structure of a peptide chain release factor 3 (prfc) from coxiella2 burnetii
28	c2z64C_	Alignment	not modelled	35.0	14	**PDB header:**immune system **Chain:** C: **PDB Molecule:**lymphocyte antigen 96; **PDBTitle:** crystal structure of mouse tlr4 and mouse md-2 complex

29	c3cnlA_	Alignment	not modelled	34.5	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of gnp-bound ylqf from t. maritima
30	c1vmeB_	Alignment	not modelled	34.3	13	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**flavoprotein; **PDBTitle:** crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
31	c3nbuC_	Alignment	not modelled	34.3	17	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of pgi glucosephosphate isomerase
32	c2elfA_	Alignment	not modelled	34.0	15	**PDB header:**translation **Chain:** A: **PDB Molecule:**protein translation elongation factor 1a; **PDBTitle:** crystal structure of the selb-like elongation factor ef-pyl2 from methanosarcina mazei
33	c3cdzA_	Alignment	not modelled	33.4	24	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**coagulation factor viii heavy chain; **PDBTitle:** crystal structure of human factor viii
34	c2j69D_	Alignment	not modelled	33.1	26	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**bacterial dynamin-like protein; **PDBTitle:** bacterial dynamin-like protein bdlp
35	d1puja_	Alignment	not modelled	33.0	36	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
36	d1ycga1	Alignment	not modelled	32.7	10	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
37	c3izq1_	Alignment	not modelled	32.5	21	**PDB header:**ribosomal protein,hydrolase **Chain:** 1: **PDB Molecule:**elongation factor 1 alpha-like protein; **PDBTitle:** structure of the dom34-hbs1-gdpnp complex bound to a translating2 ribosome
38	d1e5da1	Alignment	not modelled	31.1	10	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
39	c1g7tA_	Alignment	not modelled	29.4	22	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if2/eif5b; **PDBTitle:** x-ray structure of translation initiation factor if2/eif5b2 complexed with gdpnp
40	c2q8nB_	Alignment	not modelled	27.4	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of glucose-6-phosphate isomerase (ec2 5.3.1.9) (tm1385) from thermotoga maritima at 1.82 a3 resolution
41	d1ag9a_	Alignment	not modelled	27.2	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
42	c3degC_	Alignment	not modelled	26.5	24	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** complex of elongating escherichia coli 70s ribosome and ef4(lepa)-2 gmppnp
43	d1ykga1	Alignment	not modelled	25.7	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
44	c3ka5A_	Alignment	not modelled	25.1	40	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**ribosome-associated protein y (psrp-1); **PDBTitle:** crystal structure of ribosome-associated protein y (psrp-1)2 from clostridium acetobutylicum. northeast structural3 genomics consortium target id car123a
45	c2cmgA_	Alignment	not modelled	24.7	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**spermidine synthase; **PDBTitle:** crystal structure of spermidine synthase from helicobacter2 pylori
46	c1t10A_	Alignment	not modelled	24.5	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** phosphoglucose isomerase from leishmania mexicana in complex with2 substrate d-fructose-6-phosphate
47	c3k2tA_	Alignment	not modelled	24.4	40	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lmo2511 protein; **PDBTitle:** crystal structure of lmo2511 protein from listeria2 monocytogenes, northeast structural genomics consortium3 target lkr84a
48	d1h3ia2	Alignment	not modelled	22.8	8	**Fold:**beta-clip **Superfamily:**SET domain **Family:**Histone lysine methyltransferases
49	c3f9xA_	Alignment	not modelled	22.8	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase setd8; **PDBTitle:** structural insights into lysine multiple methylation by set2 domain methyltransferases, set8-y334f / h4-lys20me2 /3 adohcy
50	c2ywfA_	Alignment	not modelled	22.6	28	**PDB header:**translation **Chain:** A: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** crystal structure of gmppnp-bound lepa from aquifex aeolicus
51	c3h6lA_	Alignment	not modelled	22.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase setd2; **PDBTitle:** methyltransferase domain of human set domain-containing protein 2
52	d1o0ya_	Alignment	not modelled	22.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
53	d2fcra_	Alignment	not modelled	21.9	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
54	d1oboa_	Alignment	not modelled	21.7	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins

						Family: Flavodoxin-related
55	c3opeA_	Alignment	not modelled	20.9	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable histone-lysine n-methyltransferase ash1l; **PDBTitle:** structural basis of auto-inhibitory mechanism of histone2 methyltransferase
56	d1bvyf_	Alignment	not modelled	20.6	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
57	c1bvyF_	Alignment	not modelled	20.6	18	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**protein (cytochrome p450 bm-3); **PDBTitle:** complex of the heme and fmn-binding domains of the2 cytochrome p450(bm-3)
58	c1zo1I_	Alignment	not modelled	20.5	15	**PDB header:**translation/rna **Chain:** I: **PDB Molecule:**translation initiation factor 2; **PDBTitle:** if2, if1, and trna fitted to cryo-em data of e. coli 70s2 initiation complex
59	c1x5bA_	Alignment	not modelled	20.3	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**signal transducing adaptor molecule 2; **PDBTitle:** the solution structure of the vhs domain of human signal2 transducing adaptor molecule 2
60	c2bm0A_	Alignment	not modelled	20.1	21	**PDB header:**elongation factor **Chain:** A: **PDB Molecule:**elongation factor g; **PDBTitle:** ribosomal elongation factor g (ef-g) fusidic acid resistant2 mutant t84a
61	c2o2cB_	Alignment	not modelled	20.0	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase, glycosomal; **PDBTitle:** crystal structure of phosphoglucose isomerase from t. brucei2 containing glucose-6-phosphate in the active site
62	d2nqra2	Alignment	not modelled	20.0	20	**Fold:**MoeA N-terminal region -like **Superfamily:**MoeA N-terminal region -like **Family:**MoeA N-terminal region -like
63	d1c8ba_	Alignment	not modelled	19.8	20	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**HybD-like **Family:**Germination protease
64	c3mu3A_	Alignment	not modelled	19.3	14	**PDB header:**immune system **Chain:** A: **PDB Molecule:**protein md-1; **PDBTitle:** crystal structure of chicken md-1 complexed with lipid iva
65	d1ml9a_	Alignment	not modelled	19.3	46	**Fold:**beta-clip **Superfamily:**SET domain **Family:**Histone lysine methyltransferases
66	c2wu8A_	Alignment	not modelled	19.1	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** structural studies of phosphoglucose isomerase from2 mycobacterium tuberculosis h37rv
67	c3o3nB_	Alignment	not modelled	19.0	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**beta-subunit 2-hydroxyacyl-coa dehydratase; **PDBTitle:** (r)-2-hydroxyisocaproyl-coa dehydratase in complex with its substrate2 (r)-2-hydroxyisocaproyl-coa
68	d1iata_	Alignment	not modelled	18.9	18	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
69	c1s0uA_	Alignment	not modelled	18.9	18	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor 2 gamma subunit; **PDBTitle:** eif2gamma apo
70	d1pkla3	Alignment	not modelled	18.5	22	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
71	c2qv5A_	Alignment	not modelled	17.6	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu2773; **PDBTitle:** crystal structure of uncharacterized protein atu2773 from2 agrobacterium tumefaciens c58
72	c3hlyA_	Alignment	not modelled	17.5	14	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**flavodoxin-like domain; **PDBTitle:** crystal structure of the flavodoxin-like domain from2 synechococcus sp q5mzp6_synp6 protein. northeast structural3 genomics consortium target snr135d.
73	d1wu2a2	Alignment	not modelled	17.2	27	**Fold:**MoeA N-terminal region -like **Superfamily:**MoeA N-terminal region -like **Family:**MoeA N-terminal region -like
74	d1mvha_	Alignment	not modelled	17.1	31	**Fold:**beta-clip **Superfamily:**SET domain **Family:**Histone lysine methyltransferases
75	c1mvhA_	Alignment	not modelled	17.1	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cryptic loci regulator 4; **PDBTitle:** structure of the set domain histone lysine2 methyltransferase clr4
76	d1q50a_	Alignment	not modelled	16.8	13	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
77	d1nuia2	Alignment	not modelled	16.4	67	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**DNA primase zinc finger
78	c2xexA_	Alignment	not modelled	16.3	16	**PDB header:**translation **Chain:** A: **PDB Molecule:**elongation factor g; **PDBTitle:** crystal structure of staphylococcus aureus elongation factor2 g
79	d2f23a2	Alignment	not modelled	16.1	23	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
						Fold:alpha-alpha superhelix

80	d1dvpa1	Alignment	not modelled	15.6	17	**Superfamily:**ENTH/VHS domain **Family:**VHS domain
81	d1to6a_	Alignment	not modelled	15.4	18	**Fold:**Glycerate kinase I **Superfamily:**Glycerate kinase I **Family:**Glycerate kinase I
82	c3lpmA_	Alignment	not modelled	15.3	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase; **PDBTitle:** crystal structure of putative methyltransferase small domain protein2 from listeria monocytogenes
83	c2r3aA_	Alignment	not modelled	15.3	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase suv39h2; **PDBTitle:** methyltransferase domain of human suppressor of variegation2 3-9 homolog 2
84	c3oa3A_	Alignment	not modelled	15.1	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**aldolase; **PDBTitle:** crystal structure of a putative deoxyribose-phosphate aldolase from2 coccidioides immitis
85	c3o3nA_	Alignment	not modelled	15.1	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**alpha-subunit 2-hydroxyisocaproyl-coa dehydratase; **PDBTitle:** (r)-2-hydroxyisocaproyl-coa dehydratase in complex with its substrate2 (r)-2-hydroxyisocaproyl-coa
86	d1txna_	Alignment	not modelled	14.5	21	**Fold:**Coproporphyrinogen III oxidase **Superfamily:**Coproporphyrinogen III oxidase **Family:**Coproporphyrinogen III oxidase
87	d1u0fa_	Alignment	not modelled	14.1	17	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
88	c1lnsA_	Alignment	not modelled	14.1	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**x-prolyl dipeptidyl aminopetidase; **PDBTitle:** crystal structure analysis of the x-prolyl dipeptidyl2 aminopeptidase from lactococcus lactis
89	c2e59A_	Alignment	not modelled	14.0	18	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**lymphocyte antigen 96; **PDBTitle:** crystal structure of human md-2 in complex with lipid iva
90	c3by5A_	Alignment	not modelled	14.0	27	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**cobalamin biosynthesis protein; **PDBTitle:** crystal structure of cobalamin biosynthesis protein chig from2 agrobacterium tumefaciens str. c58
91	d3by5a1	Alignment	not modelled	14.0	27	**Fold:**CobE/GbiG C-terminal domain-like **Superfamily:**CobE/GbiG C-terminal domain-like **Family:**CobE/GbiG C-terminal domain-like
92	c2ftcB_	Alignment	not modelled	14.0	14	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**mitochondrial ribosomal protein l2; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome
93	c1skqB_	Alignment	not modelled	13.9	24	**PDB header:**translation **Chain:** B: **PDB Molecule:**elongation factor 1-alpha; **PDBTitle:** the crystal structure of sulfolobus solfataricus elongation2 factor 1-alpha in complex with magnesium and gdp
94	d2g50a3	Alignment	not modelled	13.7	13	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
95	d1lnsa2	Alignment	not modelled	13.5	10	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**PepX C-terminal domain-like
96	d2evra2	Alignment	not modelled	13.4	8	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**NlpC/P60
97	c2qptA_	Alignment	not modelled	13.3	24	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**eh domain-containing protein-2; **PDBTitle:** crystal structure of an ehd atpase involved in membrane remodelling
98	c3simA_	Alignment	not modelled	13.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein, family 18 chitinase; **PDBTitle:** crystallographic structure analysis of family 18 chitinase from crocus2 vernus
99	c2d6fA_	Alignment	not modelled	13.0	21	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit d; **PDBTitle:** crystal structure of glu-trna(gln) amidotransferase in the2 complex with trna(gln)